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#2 OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/965,099

DATE: 01/10/2002

TIME: 09:26:42

Input Set : N:\Crf3\RULE60\09965099.txt

Output Set: N:\CRF3\01102002\I965099.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Blackburn, Michael

6 Feuerstein, Giora

7 Patel, Arunbhai

9 (ii) TITLE OF INVENTION: ANTICOAGULANT AGENTS USEFUL IN
10 TREATMENT OF THROMBOSIS

12 (iii) NUMBER OF SEQUENCES: 111

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: SmithKline Beecham Corporation

16 (B) STREET: 709 Swedeland Road

17 (C) CITY: King of Prussia

18 (D) STATE: PA

19 (E) COUNTRY: USA

20 (F) ZIP: 19406

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Diskette

24 (B) COMPUTER: IBM Compatible

25 (C) OPERATING SYSTEM: DOS

26 (D) SOFTWARE: FastSEQ Version 1.5

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/09/965,099

C--> 30 (B) FILING DATE: 26-Sep-2001

31 (C) CLASSIFICATION:

33 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: 09/346,487

35 (B) FILING DATE:

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: Baumeister, Kirk

41 (B) REGISTRATION NUMBER: 33,833

42 (C) REFERENCE/DOCKET NUMBER: P50438-1

44 (ix) TELECOMMUNICATION INFORMATION:

45 (A) TELEPHONE: 610-270-5096

46 (B) TELEFAX:

47 (C) TELEX:

50 (2) INFORMATION FOR SEQ ID NO: 1:

52 (i) SEQUENCE CHARACTERISTICS:

53 (A) LENGTH: 20 base pairs

54 (B) TYPE: nucleic acid

55 (C) STRANDEDNESS: single

56 (D) TOPOLOGY: linear

58 (ii) MOLECULE TYPE: cDNA

59 (iii) HYPOTHETICAL: NO

60 (iv) ANTI-SENSE: NO

W--> 61 (v) FRAGMENT TYPE:

62 (vi) ORIGINAL SOURCE:

64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ENTERED

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66 CATCCTAGAG TCACCGAGGA
68 (2) INFORMATION FOR SEQ ID NO: 2: 20
69     (i) SEQUENCE CHARACTERISTICS:
70         (A) LENGTH: 21 base pairs
71         (B) TYPE: nucleic acid
72         (C) STRANDEDNESS: single
73         (D) TOPOLOGY: linear
74     (ii) MOLECULE TYPE: cDNA
75     (iii) HYPOTHETICAL: NO
76     (iv) ANTI-SENSE: NO
W--> 77     (v) FRAGMENT TYPE:
78     (vi) ORIGINAL SOURCE:
82     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
84 AGCTGCCCAA AGTGCCAAG C 21
86 (2) INFORMATION FOR SEQ ID NO: 3:
87     (i) SEQUENCE CHARACTERISTICS:
88         (A) LENGTH: 36 base pairs
89         (B) TYPE: nucleic acid
90         (C) STRANDEDNESS: single
91         (D) TOPOLOGY: linear
92     (ii) MOLECULE TYPE: cDNA
93     (iii) HYPOTHETICAL: NO
94     (iv) ANTI-SENSE: NO
W--> 95     (v) FRAGMENT TYPE:
96     (vi) ORIGINAL SOURCE:
100     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
102 CTAACACTCA TTCCTGTTGA AGCTCTTGAC AATGGG 36
104 (2) INFORMATION FOR SEQ ID NO: 4:
105     (i) SEQUENCE CHARACTERISTICS:
106         (A) LENGTH: 21 base pairs
107         (B) TYPE: nucleic acid
108         (C) STRANDEDNESS: single
109         (D) TOPOLOGY: linear
110     (ii) MOLECULE TYPE: cDNA
111     (iii) HYPOTHETICAL: NO
112     (iv) ANTI-SENSE: NO
W--> 113     (v) FRAGMENT TYPE:
114     (vi) ORIGINAL SOURCE:
118     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
120 GATTTTCARG TGCAGATTTT C 21
122 (2) INFORMATION FOR SEQ ID NO: 5:
123     (i) SEQUENCE CHARACTERISTICS:
124         (A) LENGTH: 363 base pairs
125         (B) TYPE: nucleic acid
126         (C) STRANDEDNESS: single
127         (D) TOPOLOGY: linear
128     (ii) MOLECULE TYPE: cDNA
129     (iii) HYPOTHETICAL: NO
130     (iv) ANTI-SENSE: NO

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W--> 133      (v) FRAGMENT TYPE:
134      (vi) ORIGINAL SOURCE:
136      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
138 CAGATCCAGT TGGTGCAGTC TGGACCTGAG CTGAAGAAGC CTGGAGAGAC AGTCAAGATC      60
139 TCCTGCAAGG CTTCTGGGTA CACCTTCACA AACTATGGAA TGAAGTGGGT GAAGCAGGCT      120
140 CCAGGAAAGG GTTTAAAGTG GATGGGCTGG ATAAACACCA GAAATGGAAA GTCAACATAT      180
141 GTTGATGACT TCAAGGGACG GTTGCCTTC TCTTTGGAAA GCTCTGCCAG CACTGCCAAT      240
142 TTGCAGATCG ACAACCTCAA AGATGAGGAC ACGGCTACAT ATTTCTGTAC AAGAGAAGGG      300
143 AATATGGATG GTTACTTCCC TTTACTTAC TGGGGCCAAG GGAAGTCTGGT CACTGTCTCT      360
144 GCA
146 (2) INFORMATION FOR SEQ ID NO: 6:
148      (i) SEQUENCE CHARACTERISTICS:
149          (A) LENGTH: 321 base pairs
150          (B) TYPE: nucleic acid
151          (C) STRANDEDNESS: single
152          (D) TOPOLOGY: linear
154      (ii) MOLECULE TYPE: cDNA
155      (iii) HYPOTHETICAL: NO
156      (iv) ANTI-SENSE: NO
W--> 157      (v) FRAGMENT TYPE:
158      (vi) ORIGINAL SOURCE:
160      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
162 CAAATTGTTC TCTCCAGTC TCCAGCAATC CTGTCTGCAT CTCCAGGGGA GAAGGTCACA      60
163 ATGACTTGCA GGGCCAGCTC AAGTGTAAT TACATGCACT GGTACCAGCA GAAGCCAGGA      120
164 TCCTCCCCCA AACCCTGGAT TTATGCCACA TCCAACCTGG CTTCTGGAGT CCCTGCTCGC      180
165 TTCAGTGGCA GTGGGTCTGG GACCTCTTAC TCTCTACAA TCAGCAGAGT GGAGGCTGAA      240
166 GATGCTGCCA CTTATTACTG CCAGCAGTGG AGTATTAAAC CACGGACGTT CGGTGGAGGC      300
167 ACCAAGCTGG AAATCAAACG G
169 (2) INFORMATION FOR SEQ ID NO: 7:
171      (i) SEQUENCE CHARACTERISTICS:
172          (A) LENGTH: 121 amino acids
173          (B) TYPE: amino acid
174          (C) STRANDEDNESS: single
175          (D) TOPOLOGY: linear
177      (ii) MOLECULE TYPE: peptide
178      (iii) HYPOTHETICAL: NO
179      (iv) ANTI-SENSE: NO
180      (v) FRAGMENT TYPE: internal
181      (vi) ORIGINAL SOURCE:
183      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
185 Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
186 1 5 10 15
187 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
188 20 25 30
189 Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
190 35 40 45
191 Gly Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe
192 50 55 60
193 Lys Gly Arg Phe Ala Phe Ser Leu Glu Ser Ser Ala Ser Thr Ala Asn

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194 65              70              75              80
195 Leu Gln Ile Asp Asn Leu Lys Asp Glu Asp Thr Ala Thr Tyr Phe Cys
196              85              90              95
197 Thr Arg Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr Trp Gly
198              100              105              110
199 Gln Gly Thr Leu Val Thr Val Ser Ala
200              115              120
202 (2) INFORMATION FOR SEQ ID NO: 8:
204     (i) SEQUENCE CHARACTERISTICS:
205         (A) LENGTH: 5 amino acids
206         (B) TYPE: amino acid
207         (C) STRANDEDNESS: single
208         (D) TOPOLOGY: linear
210     (ii) MOLECULE TYPE: peptide
211     (iii) HYPOTHETICAL: NO
212     (iv) ANTI-SENSE: NO
213     (v) FRAGMENT TYPE: internal
214     (vi) ORIGINAL SOURCE:
216     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
218 Asn Tyr Gly Met Asn
219 1          5
221 (2) INFORMATION FOR SEQ ID NO: 9:
223     (i) SEQUENCE CHARACTERISTICS:
224         (A) LENGTH: 17 amino acids
225         (B) TYPE: amino acid
226         (C) STRANDEDNESS: single
227         (D) TOPOLOGY: linear
229     (ii) MOLECULE TYPE: peptide
230     (iii) HYPOTHETICAL: NO
231     (iv) ANTI-SENSE: NO
232     (v) FRAGMENT TYPE: internal
233     (vi) ORIGINAL SOURCE:
235     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
237 Trp Ile Asn Thr Arg Asn Gly Lys Ser Thr Tyr Val Asp Asp Phe Lys
238 1          5          10          15
239 Gly
242 (2) INFORMATION FOR SEQ ID NO: 10:
244     (i) SEQUENCE CHARACTERISTICS:
245         (A) LENGTH: 12 amino acids
246         (B) TYPE: amino acid
247         (C) STRANDEDNESS: single
248         (D) TOPOLOGY: linear
250     (ii) MOLECULE TYPE: peptide
251     (iii) HYPOTHETICAL: NO
252     (iv) ANTI-SENSE: NO
253     (v) FRAGMENT TYPE: internal
254     (vi) ORIGINAL SOURCE:
256     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
258 Glu Gly Asn Met Asp Gly Tyr Phe Pro Phe Thr Tyr

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259   1           5           10
261 (2) INFORMATION FOR SEQ ID NO: 11:
263   (i) SEQUENCE CHARACTERISTICS:
264       (A) LENGTH: 107 amino acids
265       (B) TYPE: amino acid
266       (C) STRANDEDNESS: single
267       (D) TOPOLOGY: linear
269   (ii) MOLECULE TYPE: peptide
270   (iii) HYPOTHETICAL: NO
271   (iv) ANTI-SENSE: NO
272   (v) FRAGMENT TYPE: internal
273   (vi) ORIGINAL SOURCE:
275   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
277   Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
278       1           5           10           15
279   Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Asn Tyr Met
280       20           25           30
281   His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
282       35           40           45
283   Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
284       50           55           60
285   Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
286       65           70           75           80
287   Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Ser Ile Asn Pro Arg Thr
288       85           90           95
289   Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
290       100          105
292 (2) INFORMATION FOR SEQ ID NO: 12:
294   (i) SEQUENCE CHARACTERISTICS:
295       (A) LENGTH: 10 amino acids
296       (B) TYPE: amino acid
297       (C) STRANDEDNESS: single
298       (D) TOPOLOGY: linear
300   (ii) MOLECULE TYPE: peptide
301   (iii) HYPOTHETICAL: NO
302   (iv) ANTI-SENSE: NO
303   (v) FRAGMENT TYPE: internal
304   (vi) ORIGINAL SOURCE:
306   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
308   Arg Ala Ser Ser Val Asn Tyr Met His
309       1           5           10
311 (2) INFORMATION FOR SEQ ID NO: 13:
313   (i) SEQUENCE CHARACTERISTICS:
314       (A) LENGTH: 7 amino acids
315       (B) TYPE: amino acid
316       (C) STRANDEDNESS: single
317       (D) TOPOLOGY: linear
319   (ii) MOLECULE TYPE: peptide
320   (iii) HYPOTHETICAL: NO

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/965,099

DATE: 01/10/2002

TIME: 09:26:43

Input Set : N:\Crif3\RULE60\09965099.txt

Output Set: N:\CRF3\01102002\I965099.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:61 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=1
L:79 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=2
L:97 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=3
L:115 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=4
L:133 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=5
L:157 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=6
L:360 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=15
L:379 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=16
L:398 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=17
L:417 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=18
L:436 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=19
L:518 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=21
L:536 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=22
L:554 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=23
L:606 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=25
L:625 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=26
L:643 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=27
L:661 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=28
L:680 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=29
L:699 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=30
L:786 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=32
L:806 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=33
L:826 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=34
L:901 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=36
L:919 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=37
L:937 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=38
L:988 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=40
L:1006 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=41
L:1024 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=42
L:1042 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=43
L:1123 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=45
L:1143 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=46
L:1163 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=47
L:1232 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=49
L:1250 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=50
L:1268 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=51
L:1355 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=53
L:1374 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=54
L:1414 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=56
L:1495 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=58
L:1513 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=59
L:1550 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=61
L:1631 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=63
L:1651 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=64
L:1671 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=65
L:1746 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=67

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L:1764 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=68
L:1782 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=69
L:1820 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=71
L:1838 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=72